Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: DAVID GUZO   Examiner #: 70677 Date: 8/11/05

Art Unit: 1636   Phone Number: 2-0767   Serial Number: 10/695243

Location (Bldg/Room#): 2A74 (Mailbox #): 2C70 Results Format Preferred (circle) (PAPER) DISK

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Date: _____

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please run a regular and interference sequence search
on SEQ ID NO: 1 and 3.

1 NA 1389   Thanks

nej   3 NA 1389

LM

CRFS

ACCESS DB # _163705_

PLEASE PRINT CLEARLY

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: _DAVID GUZO_   Examiner # : _70677_   Date: _8/24/05_

Art Unit: _1636_   Phone Number: _2-0767_   Serial Number: _10/695243_

Location (Bldg/Room#): _Remsen_   (Mailbox #): _2C70_   Results Format Preferred (circle): PAPER   DISK
_2A75_

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

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_____

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Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search for nuclear acid sequences which encode a polypeptide at least 77% identical to SEQ ID NO:2 or 4.

2 aa 462

Mej   4 aa 462

200 Hits }
50 align } 1ˢᵗ pass

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 28, 2005, 14:09:22 ; Search time 730.5 Seconds
(without alignments)
3743.902 Million cell updates/sec

Title: US-10-695-243-4
Perfect score: 2510
Sequence: 1 MAXFRRTCILLSLFILFIP.........SEKFSKERMTYALDLQOOPAS 462

Scoring table: BLOSUM62
    Xgapop 10.0 ; Xgapext 0.5
    Ygapop 10.0 ; Ygapext 0.5
    Fgapop 6.0 ; Fgapext 7.0
    Delop 6.0 ; Delext 7.0

Searched: 4390206 seqs, 295987067 residues

Total number of hits satisfying chosen parameters: 8780412

Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
    Maximum Match 100%
    Listing first 200 summaries

Command line parameters:
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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10695243/runat_26082005_123021_16577/app_query.fasta_1.1294
-DB=N Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCt=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=200 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10695243 @CGN_1_957 @runat_26082005_123021_16577 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :
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 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2004ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2510	100.0	1389	13	ADR46940	Adr46940 Mouse end
2	2176	86.7	3762	10	ADI21896	Adi21896 Novel hum
3	2176	86.7	4386	10	ABV23530	Abv23530 Human pro
4	2176	86.7	4386	5	ABV29386	Abv29386 Human pro
5	2170	86.5	1389	13	ADR46938	Adr46938 Human liv
6	2118	84.4	4603	4	AAD08491	Aad08491 Human sec
7	1814	72.3	4320	8	ABA00835	Aba00835 Carbohydr
8	1777	70.8	2388	8	AAH17709	Aah17709 Human end
9	1469	58.5	2310	8	ABX70915	Abx70915 Novel hum
10	1414	56.3	1194	10	ADC26272	Adc26272 Human NOV
11	1259	50.2	2098	5	ABA05943	Aba05943 Human end
12	1247	49.7	2175	3	AAC79978	Aac79978 Human sec
13	1185	47.2	1840	12	ADO21136	Ado21136 Human cod
14	948	37.8	2341	10	ADA53117	Ada53117 Human car
15	795	31.7	507	12	ACH78012	Ach78012 Human gen
16	741	29.5	713	10	ADE54765	Ade54765 Rat gene
17	518	20.6	584	5	ABV44623	Abv44623 Human pro
18	518	20.6	348	4	ABV35823	Abv35823 Human pro
19	513	20.4	1380	4	AAH06030	Aah06030 Human CDN
20	420.5	16.8	550	4	ABI24141	Abi24141 Drosophil
21	390	15.5	550	12	ACH91730	Ach91730 Human gen
22	366	14.6	3651	4	ABL24140	Abl24140 Drosophil
23	341	13.6	449	6	ABV05577	Abv05577 Human pro
24	235	9.4	507	10	ACD95012	Acd95012 Human col
25	224.5	8.9	2297	12	ABI24142	Abi24142 Drosophil
26	214	8.5	920	6	ACA24531	Aca24531 Prokaryot
27	214	8.5	920	6	ABN35307	Abn35307 Human spl
28	193	7.7	920	6	ABL37966	Abl37966 Human col
29	193	7.7	920	6	ACA30982	Aca30982 Prokaryot
30	141.5	5.6	3081	8	ABZ59024	Abz59024 Prunus se
31	126	5.0	516	6	ABL61255	Abl61255 S. mutans
32	125.5	5.0	60	6	ABL61252	Abl61252 S. mutans
33	119	4.7	2787	4	ABL61256	Abl61256 S. mutans
34	117	4.7	2367	6	ABL61254	Abl61254 S. mutans
35	115	4.6	2356	6	ABL61253	Abl61253 S. mutans
36	114.5	4.6	3092	8	ABL61251	Abl61251 S. mutans
37	113	4.5	2998	9	ABL32266	Abl32266 Human imm
38	110	4.4	2037	6	AAC47189	Aac47189 Arabidops
39	110	4.4	2169	6	ABQ70972	Abq70972 Listeria
40	110	4.4	2235	6	ABQ97421	Abq97421 Listeria
41	110	4.4	2256	6	ABZ32546	Abz32546 Candida a
42	110	4.4	2367	6	AAS82190	Aas82190 DNA encod
43	110	4.4	2388	6	ABZ34699	Abz34699 Coding se
44	110	4.4	6419	3	AAH62689	Aah62689 Shrimp wh
45	108	4.4	1963	3	ADA89728	Ada89728 Staphyloc
46	108	4.3	5917	6	ADB53839	Adb53839 Primary r
47	107.5	4.3	228835	12	ABT14992	Abt14992 Pathogen
48	107	4.3	1434	5	ABN91416	Abn91416 Staphyloc
49	107	4.3	8062	5	ADS02700	Ads02700 Staphyloc
50	106.5	4.2	2678	4	ADP71342	Adp71342 DNA seque
51	106.5	4.2	4311	4	AAF62021	Aaf62021 E. canis
52	106.5	4.2	2305	4	ABQ61152	Abq61152 MUCSB par
53	106	4.2	305107	4	ADS45595	Ads45595 Bacterial
54	104.5	4.2	2661	10	ACA48172	Aca48172 Prokaryot
55	104.5	4.2	4005	8	ABN66673	Abn66673 Streptoco
56	104.5	4.2	4008	13	ADS47281	Ads47281 Bacterial
57	104.5	4.2	4008	11	ACF70956	Acf70956 Photorhab
58	104.5	4.2	5299	11	AAV13173	Aav13173 Complete
59	104.5	4.2	5300	5	AAV13172	Aav13172 Complete
60	104.5	4.2	13715	6	ACF67367_40	Acf67367_40 Continuation (41 o
61	104	4.1	1515	13	ACF65388_07	Acf65388_07 Continuation (8 of
62	104	4.1	2385	8	ABX63458	Abx63458 Human cDN
63	104	4.1	3504	6	ADQ84327	Adq84327 Human tum
64	104	4.1	9240	13	ACN40587	Acn40587 Tumour-as
65	103.5	4.1	1647	10	ABN97367	Abn97367 Gene #386
66	103.5	4.1	1647	8	ADP75180	Adp75180 Human End
67	103.5	4.1	4009	2	ADM03385	Adm03385 Human CDN
68	103.5	4.1	1110000	10	AAA61145	Aaa61145 SEN virus
69	103.5	4.1	1110000	10	AAA61154	Aaa61154 SEN virus
70	103	4.1	1740	8	AAA61144	Aaa61144 SEN virus
71	103	4.1	1741	10		
72	103	4.1	1743	6		
73	103	4.1	304905	11		
74	102.5	4.1	1952	11		
75	102.5	4.1	2259	3		
76	102.5	4.1	2259	3		
77	102.5	4.1	2609	3		
78	102.5	4.1	3313	3		

OM protein - nucleic search, using frame_plus_p2n model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: August 28, 2005, 14:11:42 ; Search time 6175.5 Seconds
(without alignments)
3625.020 Million cell updates/sec

Title: US-10-695-243-2
Perfect score: 2501
Sequence: 1 MAKFRRTCIIIALPILPIF..........SEKYSKERATYALDRQLPVS 462

Scoring table: BLOSUM62
Xgapop 10.0 ; Xgapext 0.5
Ygapop 10.0 ; Ygapext 0.5
Fgapop 6.0 ; Fgapext 7.0
Delop 6.0 ; Delext 7.0

Searched: 4708233 seqs, 2427607955 residues

Total number of hits satisfying chosen parameters: 9416466

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:
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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=200
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US10695243_@CGN_1.1_7837 @runat_26082005_123021_16586 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2501	100.0	1389	6	CQ868818	CQ868818 Sequence
2	2501	100.0	4596	6	HSM806986	BX640869 Homo sapi
3	2497	99.8	4386	6	CQ491652	CQ491652 Sequence
4	2497	99.8	4386	6	CQ497537	CQ497537 Sequence
5	2492	99.6	1474	9	HSA577574	HSA577574 Homo sapi
6	2490	99.6	4558	10	HSM806695	BX537398 Homo sapi
7	2180	87.2	4645	10	BC067076	BC067076 Mus muscu
8	2170	86.8	1389	5	CQ868820	CQ868820 Sequence
9	1972	78.8	2552	6	AF023657	AF023657 Rattus no
10	1962	78.4	2310	10	BD159701	BD159701 Primer fo
11	1962	78.4	2388	6	AX822397	AX822397 Sequence
12	1962	78.4	2388	6	AK022900	AK022900 Xenopus 1
13	1699	67.9	2779	5	BC077304	BC077304 Xenopus 1
14	1669	66.7	1408	9	CR354351	CR354351 Tetraodon
15	1458.5	58.3	2770	10	BC065047	BC065047 Mus muscu
16	1447	57.9	2310	6	AR541894	AR541894 Sequence
17	1401	56.0	1083	6	CQ722353	CQ722353 Sequence
18	1305.5	52.2	1299	6	AC110674	AC110674 Danio rer
19	1199.5	48.0	3286	5	BC081681	BC081681 Danio rer
20	1178	47.1	1859	6	BC063587	BC063587 Homo sapi
21	1176	47.0	105273	9	AL671884	AL671884 Human DNA
22	1093	43.7	782	9	AY048774	AY048774 Homo sapi
23	1077	43.1	256771	2	AC115326	AC115326 Rattus no
24	1058	42.3	193704	10	AL805949	AL805949 Mouse DNA
25	1006	40.2	2120	9	BC077730	BC077730 Homo sapi
26	1006	40.2	2338	9	AB188490	AB188490 Homo sapi
27	1006	40.2	1096	9	AY048775	AY048775 Homo sapi
28	985	39.4	2341	6	AX714001	AX714001 Sequence
29	949	37.9	2341	6	AK055996	AK055996 Homo sapi
30	949	37.9	713	9	CQ482870	CQ482870 Sequence
31	899	35.9	2341	6	AC142187	AC142187 Rattus no
32	852	34.1	181070	2	AB016942	AB016942 Bacteroid
33	851	34.0	301630	1	AC104336	AC104336 Homo sapi
34	845	33.8	134161	9	AL929472	AL929472 Human DNA
35	845	33.8	143060	9	AC022557	AC022557 Homo sapi
36	845	33.8	170908	2	AC023225	AC023225 Homo sapi
37	845	33.8	190310	2	AL513473	AL513473 Homo sapi
38	845	33.8	255952	2	AC016516	AC016516 Homo sapi
39	842.5	33.7	1777067	2	AL606933	AL606933 Mouse DNA
40	841.5	33.3	58345	2	AY071523	AY071523 Drosophil
41	835	33.4	197552	10	CQ473701	CQ473701 Drosophil
42	702	28.1	781	6	CQ605694	CQ605694 Sequence
43	664	26.5	584	6	CQ722373	CQ722373 Sequence
44	664	26.5	584	6	CQ503974	CQ503974 Sequence
45	662	26.5	1347	5	CQ512775	CQ512775 Homo sapi
46	587	23.5	1246	5	BC009952	BC009952 Sequence
47	569	22.8	67717	2	BX930133	BX930133 Gallus ga
48	553	22.1	348	6	AC101393	AC101393 Mus muscu
49	553	22.1	1075	6	BD148022	BD148022 Primer fo
50	535.5	21.4	348	6	AX867960	AX867960 Sequence
51	519	20.8	797	9	BC038190	BC038190 Homo sapi
52	504	20.2	1357	6	BV174680	BV174680 Sqnm73513
53	467	18.7	449	6	BC031903	BC031903 Homo sapi
54	415	16.6	2136	3	CQ473701	CQ473701 Homo sapi
55	395	15.8	1380	3	AY071523	AY071523 Homo sapi
56	389	15.6	190310	2	CQ737701	CQ737701 Drosophil
57	348	13.9	44117	2	CQ605693	CQ605693 Sequence
58	348	13.9	3651	6	CO605693	CO605693 Sequence
59	346	13.8	164884	3	AC011063	AC011063 Homo sapi
60	346	13.8	193924	3	AC009910	AC009910 Drosophil
61	346	13.8	260249	3	AE003610	AE003610 Drosophil
62	262	10.5	673	6	AR508592	AR508592 Sequence
63	246	9.8	622	11	BV022021	BV022021 S21P26018
64	246	9.8	347800	1	AP000060	AP000060 Aeropyrum
65	188.5	7.5	685	9	HSA334442	HSA334442 Homo sapi
66	178.5	7.1	600	9	HSA334516	HSA334516 Homo sapi
67	178	7.1	861	9	HSA334462	HSA334462 Homo sapi
68	176.5	7.1	753	9	HSA302260	HSA302260 Homo sapi
69	170	6.8	826	9	HSA336605	HSA336605 Homo sapi
70	170	6.8	167000	1	AP000059	AP000059 Aeropyrum
71	149.5	5.9	300254	1	AB016933	AB016933 Bacteroid
72	146.5	5.9	236120	14	AF063866	AF063866 Melanoplu
73	140	5.6	516	6	AX341307	AX341307 Sequence
74	138	5.5	349980	6	AX345557	AX345557 Sequence
75	135.5	5.4	10317	1	AE005739	AE005739 Caulobact
76	130	5.2	60	6	CQ538420	CQ538420 Plasmodiu
77	125.5	5.0	169546	2	AC004157	AC004157 Bacteroid
78	125.5	5.0	302605	1	AE016938	AE016938 Bacteroid